

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 10:13:33 ; Search time 95.3285 Seconds
(without alignments)
10583.354 Million cell updates/sec

Title: US-09-922-895-4

Perfect score: 448
Sequence: 1 TAGGTGAGATGCAGAAAATT.....CCCTGCTATATGAAGCCTT 448

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
- 24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	100.0	1717	24	ABL67066
2	448	100.0	1717	24	AAD25221
3	448	100.0	1717	24	AAD25245
4	448	100.0	1915	18	AAT85162
5	448	100.0	5099	18	AAT93601
6	380.4	84.9	1689	17	AAT31334
7	380.4	84.9	1689	18	AAT58783
8	380.4	84.9	1689	19	AAV07402
9	380.4	84.9	1689	21	AAF21268

10	380.4	84.9	1689	21	AAA35146
11	380.4	84.9	1689	24	ABL40462
12	380.4	84.9	3958	21	AAF21269
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14	339.2	75.7	7201	24	ABL32337
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18	105	23.4	1201	24	ABK84282
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21	43	9.6	1348	22	AAH74716
22	42.2	9.4	2865	22	AAS46320
23	42.2	9.4	2865	24	ABN80051
24	42.2	9.4	5269	24	ABL34056
25	42.2	9.4	9905	24	ABL32063
26	42	9.4	18512	24	ABL32976
27	42	9.4	33053	24	ABQ67005
28	41.6	9.3	6078	22	AAS46405
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32	41.6	9.3	17294	24	ABL32986
33	41.4	9.2	19459	24	ABL70527
34	41.4	9.2	19459	24	ABK31212
35	41.2	9.2	15548	24	ABL34155
36	41.2	9.2	83391	24	ABQ67093
37	41	9.2	498	24	ABN92804
38	41	9.2	2908	22	AAH54995
39	40.8	9.1	375	22	AAF65616
40	40.8	9.1	379	22	AAF65615
41	40.8	9.1	10467	24	ABL49302
42	40.8	9.1	12601	24	ABL34207
43	40.6	9.1	3524	23	ABL26502
44	40.6	9.1	6621	24	ABL70156
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ALIGNMENTS

RESULT 1	ABL67066	standard; DNA: 1717 BP.
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AC	ABL67066;	
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DT	15-MAY-2002	(first entry)
XX		
DE	Thyroid cancer related gene sequence SEQ ID NO:5403.	
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KW	Human; Cancer: colon; breast; ovary; oesophagus; kidney; thyroid;	
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;	
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;	
KW	gene; ds.	
OS	Homo sapiens.	
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PN	W0200194629-A2.	
XX		
PD	13-DEC-2001.	
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PF	30-MAY-2001; 2001WO-US10838.	
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PR	05-JUN-2000; 2000US-209473P.	
PR	05-JUN-2000; 2000US-209531P.	
PR	18-SEP-2000; 2000US-233133P.	
PR	18-SEP-2000; 2000US-233617P.	
PR	20-SEP-2000; 2000US-234009P.	
PR	20-SEP-2000; 2000US-234034P.	
PR	20-SEP-2000; 2000US-234052P.	
PR	22-SEP-2000; 2000US-234509P.	
PR	22-SEP-2000; 2000US-234567P.	

Human adenosine re
Human C-C chemok
Human low adenosin
Human adenosine re
Human immune syste
Human immune syste
Human low adenosin
Human adenosine re
Human cDNA differe
Human chemically p
Chemically pretrea
Nucleotide sequenc
Tumour suppressor
Human chemically m
Human immune syste
Human immune syste
Human angiotensin
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Tumour suppressor
Human immune syste
Human chemically p
Human immune syste
Human immune syste
Chemically treated
Signal transductio
Human immune syste
Human angiogenesis
Staphylococcus epi
S. epidermidis gen
Novel human polynu
Novel human polynu
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Drosophila melanog
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Human DNA for stag

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 XX
 PA (AVAL-) AVALON PHARM.
 XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 DR WPI: 2002-188264/24.

PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set -
 XX
 XX

Claim 1; SEQ ID 5403; 44pp; English.

XX The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in AB161664
 CC to AB170110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytosolic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilms' tumour.
 XX
 XX

Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 other;

Query Match 100.0%; Score 448; DB 24; Length 1717;
 Best Local Similarity 100.0%; Pred. No. 7.8e-105;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1390 TTGAGACACTGAAATATATACACACAGCAGTAGAGATGATGATGACCTTAAGTCAATT 1449
 QY 181 ACCACAGGCCAGGGGCTGGGACGCTACTGATCATCAACCTTAAGCAAGAGCTTGGCT 240
 DB 1450 ACCACAGGCCAGGGGCTGGGACGCTACTGATCATCAACCTTAAGCAAGAGCTTGGCT 1509
 QY 241 TCTCTCTCTAAATGAGTACCTATTTAATGACCGTGAATGATGATGATGATGATGATGAT 300
 DB 1510 TCTCTCTCTAAATGAGTACCTATTTAATGACCGTGAATGATGATGATGATGATGATGAT 1569
 QY 301 TGGCGCTACAAAAGGTAAGCTTTTATATTTTATATATTAATTAATTAATTAATTAATTAAT 360
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 QY 361 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
 DB 1630 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1689
 QY 421 AGTTCTTCCCTGCTTAATGAAGGCTT 448
 DB 1690 AGTTCTTCCCTGCTTAATGAAGGCTT 1717

RESULT 2
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 ID AAD25221 standard; DNA; 1717 BP.

XX AAD25221;

DT 12-MAR-2002 (first entry)

XX Human chemokine (C-C motif) receptor 3 (CCR3) gene #1.

KW Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;
 KW genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;
 KW human immunodeficiency virus 1; single nucleotide polymorphism; SNP;
 KW chromosome 3p21.3; ds.
 XX
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OS Homo sapiens.

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XX WO200187908-A2.

XX 22-NOV-2001.

XX 18-MAY-2001; 2001WO-US16278.

XX 18-MAY-2000; 2000US-205191P.

```
XX (GENA-) GENAISANCE PHARM INC.
PA
XX
XX Choi JY, Kazemi A, Koshy B;
PI
XX
XX WPI: 2002-055681/07.
DR
XX P-PSDB: AAE15320.
XX
XX Isolated polymorphic variants of chemokine (C-C motif) receptor 3
PT (CCR3) gene useful for studying function of CCR3, expressing the CCR3
PT protein and to screen drugs to treat CCR3 activity-related diseases -
PS
XX Example 1: Fig 1: 53pp; English.
XX
XX The invention relates to genetic variants of human chemokine (C-C motif)
CC receptor 3 (CCR3) gene. The invention also relates to compositions and
CC methods for haplotyping and/or genotyping the CCR3 gene in an individual.
CC Polynucleotides of the invention are useful for studying the expression
CC and function of CCR3 and in expressing CCR3 proteins for use in screening
CC candidate drugs to treat diseases related to CCR3 activity. They are also
CC used in gene therapy. The polymorphism and haplotype data is useful for
CC validating whether CCR3 is a suitable target for drugs to treat type IV
CC hypersensitivity reactions and human immunodeficiency virus (HIV)-1,
CC screening for such drugs and reducing bias cells in clinical trials of
CC such drugs. The genotyping method is useful for determining whether an
CC individual has one haplotype or haplotype pairs. The haplotyping method
CC is useful for improving the efficiency and outcome of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.
CC The present sequence is human CCR3 gene located on chromosome 3p21.3.
XX
XX Sequence 1717 BP; 434 A; 428 C; 351 G; 504 T; 0 other:
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Query Match 100.0%; Score 448; DB 24; Length 1717;
Best Local Similarity 100.0%; Pred. No. 7.8e-105;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1270 TAGGTGACATGACAGAAATTTGCTTAAGAGAGAGACAGAGATGAGCAACACATT 1329
OY 61 AAGCTTCCACACTCAGCTCTTAAACAGTCTCTTCAAACTTCAGTGCACACTGAAGCTC 120
DB 1330 AAGCTTCCACACTCAGCTCTTAAACAGTCTCTTCAAACTTCAGTGCACACTGAAGCTC 1389
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DB 1390 TTGAAGACACGTAATATATACACAGCACTAGTACAGTACCTTAAGTGCATT 1449
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DB 1570 TGCAGGTACAAAAGGTAAACTTTTATATTTTATCTTACTACTACCGCATTTA 1629
OY 361 TATAAATAAACAATTTTTCACACATATACATTAAGTAACTATTTTCTATATGCTCT 420
DB 1630 TATAAATAAACAATTTTTCACACATATACATTAAGTAACTATTTTCTATATGCTCT 1689
OY 421 AGTCTTTTCCCTGCTTTAATGAAGCTT 448
DB 1690 AGTCTTTTCCCTGCTTTAATGAAGCTT 1717
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XX AAD25245;
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XX 12-MAR-2002 (first entry)
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XX Human chemokine (C-C motif) receptor 3 (CCR3) gene #2.
DE
XX
XX Human: chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping;
KM genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy;
KM human immunodeficiency virus 1; polymorphism; chromosome 3p21.3; ds.
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XX WO200187908-A2.
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XX 22-NOV-2001.
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XX 18-MAY-2001; 2001WO-US16278.
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XX 18-MAY-2000; 2000US-205191P.
XX
XX (GENA-) GENAISANCE PHARM INC.
XX
XX Choi JY, Kazemi A, Koshy B;
XX
XX WPI: 2002-055681/07.
XX
XX Isolated polymorphic variants of chemokine (C-C motif) receptor 3
PT (CCR3) gene useful for studying function of CCR3, expressing the CCR3
PT protein and to screen drugs to treat CCR3 activity-related diseases -
PS
XX
XX Claim 5: Page 53; 53pp; English.
XX
XX The invention relates to genetic variants of human chemokine (C-C motif)
CC receptor 3 (CCR3) gene. The invention also relates to compositions and
CC methods for haplotyping and/or genotyping the CCR3 gene in an individual.
CC Polynucleotides of the invention are useful for studying the expression
CC and function of CCR3 and in expressing CCR3 proteins for use in screening
CC candidate drugs to treat diseases related to CCR3 activity. They are also
CC used in gene therapy. The polymorphism and haplotype data is useful for
CC validating whether CCR3 is a suitable target for drugs to treat type IV
CC hypersensitivity reactions and human immunodeficiency virus (HIV)-1,
CC screening for such drugs and reducing bias cells in clinical trials of
CC such drugs. The genotyping method is useful for determining whether an
CC individual has one haplotype or haplotype pairs. The haplotyping method
CC is useful for improving the efficiency and outcome of several steps in
CC the discovery and development of drugs for treating diseases associated
CC with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.
CC The present sequence is human CCR3 gene located on chromosome 3p21.3.
XX
XX Sequence 1717 BP; 434 A; 427 C; 350 G; 502 T; 4 other:
SQ
Query Match 100.0%; Score 448; DB 24; Length 1717;
Best Local Similarity 100.0%; Pred. No. 7.8e-105;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1270 TAGGTGAGATGCGAAGAAATTTGCTTAAAGAGGAAGACCAAGAGATGAAACAAACATTT 1329
QY 61 AAGCCTTCACACATCAGCTCTTAAACAGTCCCTCAAACTTCCAGTGCACACATGGAAGCTC 120
XX |||||||
PS |||||||
Db 1330 AAGCCTTCACACATCAGCTCTTAAACAGTCCCTCAAACTTCCAGTGCACACATGGAAGCTC 1389
QY 121 TTGAAGACACAGTGAATATACACACAGCAGTACAGTATGATGATGATGATGATGATGATGAT 180
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PS |||||||
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PS |||||||
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XX |||||||
PS |||||||
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PS |||||||
Db 1690 AGTTCTTCCCTGCTTAATGAAAAAGCTT 1717

RESULT 4
AAT85162
ID AAT85162 standard; cDNA; 1915 BP.
XX
AC AAT85162;
XX
DT 14-DEC-1997 (first entry)
XX
DE Human chemokine receptor 88-2B cDNA.
XX
KW Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis;
KW tumour; asthma; viral infection; AIDS; inflammation;
KW autoimmune disease; therapy; diagnosis; leukocyte trafficking;
KW G protein coupled receptor; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /tag= a
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PN WO9722698-A2.
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PD 26-JUN-1997.
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PF 20-DEC-1996; 96WO-US20759.
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PR 07-JUN-1996; 96US-0661393.
PR 20-DEC-1995; 95US-0575967.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray PW, Raport CJ, Schweickart VL;
XX
DR WPI: 1997-341689/31.
DR P-PSDB; AAM27124.
XX
PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used
PT to modulate leukocyte trafficking, e.g. for treatment of
```

```
PT inflammation, tumours, viral infections, autoimmune diseases, etc.
XX
XX Claim 7; Page 48-50; 65pp; English.
PS
CC This sequence comprises a full-length cDNA coding for novel human
CC chemokine receptor 88-2B (AAM27124), a G protein coupled receptor that
CC is involved in leukocyte trafficking. The 88-2B cDNA was obtained
CC from a macrophage cDNA library using 88-2B-specific primers. A
CC full-length clone (see AAT85161) for chemokine receptor 88C (AAM27123)
CC was also obtained. 88C and 88-2B cDNAs can be used to produce
CC recombinant polypeptides in transformed host cells for use in the
CC treatment of e.g. atherosclerosis, rheumatoid arthritis, tumours,
CC asthma, viral infection, AIDS and inflammatory conditions. Nucleic
CC acid fragments can be used to isolate genomic sequences, to detect
CC alleles of the gene (for diagnosis or in gene therapy), to alter
CC receptor genetics to facilitate identification of modulators and to
CC produce knockout animals, and (antisense forms) to alter/study the
CC genetics and expression of the receptor.
XX
SQ Sequence 1915 BP; 488 A; 470 C; 373 G; 584 T; 0 other;

Query Match 100.0%; Score 448; DB 18; Length 1915;
Best Local Similarity .100.0%; Pred. No. 8.1e-105;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PS |||||||
Db 1727 TGCCGCTACAAAAAGGTAAACCTTTTATATTTTATATTAACCTTCAGCCAGCTATTTGA 1786
QY 361 TATTAATTAACATTTTTCACACATATCAATTAATTTTATTTCTAATGTCCT 420
XX |||||||
PS |||||||
Db 1787 TATTAATTAACATTTTTCACACATATCAATTAATTTTATTTCTAATGTCCT 1846
QY 421 AGTTCTTCCCTGCTTAATGAAAAAGCTT 448
XX |||||||
PS |||||||
Db 1847 AGTTCTTCCCTGCTTAATGAAAAAGCTT 1874

RESULT 5
AAT93601
ID AAT93601 standard; cDNA; 5099 BP.
XX
AC AAT93601;
XX
DT 07-MAY-1998 (first entry)
XX
DE Human eosinophil eotaxin receptor CC CKR3 encoding cDNA.
XX
KW Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis;
KW atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;
KW beta-chemokine receptor; viral infection; ss.
XX
OS Homo sapiens.
```

```
XX Key Location/Qualifiers
FH misc_feature 1..3586
FT /*tag= a
FT /note= "5' genomic DNA flanking sequence"
FT CDS 3587..4654
FT /*tag= b
FT /product= "human eosinophil ectaxin receptor"
FT misc_feature 4655..5099
FT /*tag= C
FT /note= "terminator region"
PN WO9741154-A1.
XX 06-NOV-1997.
PD 24-APR-1997; 97WO-US06568.
XX 17-JAN-1997; 97GB-0000894.
PR 26-APR-1996; 96US-0016158.
PR 26-APR-1996; 96US-0017113.
XX (MERI ) MERCK & CO INC.
PI Daugherty BL, Demartino JA, Siciliano SJ, Springer MS;
XX WPI: 1997-549685/50.
DR P-PSDB; AAM31850.
XX New isolated human eosinophil ectaxin receptor - used to develop
PT products for treating and preventing atopic conditions e.g. allergic
PT rhinitis, dermatitis, conjunctivitis and bronchial asthma
XX Claims 12, 13, 14: Pages 16-20; 51pp: English.
PS
XX This cDNA encodes a human eosinophil ectaxin receptor. This 5099 base
CC pair sequence comprises a 1065 base pair open reading frame encoding a
CC 355 amino acid eosinophil ectaxin receptor protein, flanked by a 5'
CC genomic DNA sequence and a 3' terminator region. This novel eosinophil
CC ectaxin receptor is a human beta-chemokine receptor designated CC CKR3.
CC Agents which bind to this eosinophil ectaxin receptor can be used for
CC the treatment and prevention of atopic conditions such as allergic
CC rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which
CC block this eosinophil ectaxin receptor can be used to prevent viral
CC infection in healthy individuals and slow or halt viral progression
CC in infected patients.
XX
XX Sequence 5099 BP; 1388 A; 1171 C; 1013 G; 1527 T; 0 other;
SQ
Query Match 100.0%; Score 448; DB 18; Length 5099;
Best Local Similarity 100.0%; Pred. No. 1,1e-104;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TAGGTGATGAGGAAATTTGCTTAAGAGGAGGAGGAGATGGAAGCAACATTT 60
DB 4652 TAGGTGATGAGGAAATTTGCTTAAGAGGAGGAGGAGATGGAAGCAACATTT 4711
OY 61 AAGCTTCCACACTGACCTCTTAAACAGTCTTCAAACTTCCAGTGCACACTGAAGCTC 120
DB 4712 AAGCTTCCACACTGACCTCTTAAACAGTCTTCAAACTTCCAGTGCACACTGAAGCTC 4771
OY 121 TTGAAGACACTGAATATACACAGAGAGTACAGTACAGTACAGTACCTTAAGTCAATT 180
DB 4772 TTGAAGACACTGAATATACACAGAGTACAGTACAGTACAGTACCTTAAGTCAATT 4831
OY 181 ACCACAGGCGCAGGGGCTGGGAGCTACTCATCATCAACCCCTAAAGAAGAGAGCTTTGGCT 240
DB 4832 ACCACAGGCGCAGGGGCTGGGAGCTACTCATCATCAACCCCTAAAGAAGAGAGCTTTGGCT 4891
OY 241 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACAGCTGAAATGTTAGTACTACTATA 300
DB 4892 TCTCTCTCTAAATGAGTTACCTACATTTTAATGACAGCTGAAATGTTAGTACTACTATA 4951
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OY 301 TGCGGCTACAAAAGGTAAACCTTTTATATATTTATACATTACCTCAGCCAGCTATTGA 360
DB 4952 TGCGGCTACAAAAGGTAAACCTTTTATATATTTATACATTACCTCAGCCAGCTATTGA 5011
OY 361 TATAAATTAACATTTTCCACACATACATACATTAAGTTAACTATTATTCTTAATGTGCTT 420
DB 5012 TATAAATTAACATTTTCCACACATACATACATTAAGTTAACTATTATTCTTAATGTGCTT 5071
OY 421 AGTCTCTTCCCTGCTTAATGAAGCTT 448
DB 5072 AGTCTCTTCCCTGCTTAATGAAGCTT 5099
RESULT 6
AAT31334
ID AAT31334 standard; DNA; 1689 BP.
XX
XX AAT31334;
AC 15-NOV-1996 (first entry)
DT
XX CC-chemokine receptor 3 genomic DNA.
DE
XX CC-chemokine receptor 3; CKP-3; Eos-L2; Inhibitor; antisense;
KW antiinflammatory; eosinophil; ds.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 181..1248
FT /*tag= a
FT variation 1007..1008
FT /*tag= b
FT /note= "CCR-3 genomic clone has CG at positions
FT 1007-1008, coding for threonine (ACG) at
FT position 276; a cDNA clone has GC at
FT these positions, coding for serine (AGC)"
FT misc_difference 1291
FT /*tag= c
FT /note= "base n at position 1291 is not identified
FT in the specification"
FT
FT WO9622371-A2.
XX 25-JUL-1996.
XX
XX 19-JAN-1996; 96WO-US00608.
XX
XX 19-JAN-1995; 95US-0375199.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX (LEOK-) LEUKOSITE INC.
XX
XX Gerard CJ, Gerard NP, Mackay CR, Ponath PD, Post TW;
PI Qin S;
XX
XX WPI: 1996-354528/35.
DR P-PSDB; AAM03376.
XX
XX Mammalian chemokine receptor-3 and related nucleic acids - useful to
PT identify receptor inhibitors to treat inflammatory disease, e.g.
PT autoimmune disorders, certain cancers, etc.
XX
XX Claim 1: Page 109; 153pp; English.
XX
XX A genomic DNA clone (T31334) codes for a novel receptor (W03376),
CC designated Eos L2 or C-C chemokine receptor 3 (CCR-3). Involved
CC in leukocyte migration associated with inflammation. It was
CC isolated from a human genomic library in EMBL3 SP7/T7 vector by
CC screening with a PCR fragment generated from eosinophil cDNA
CC using degenerate primers (see also T31337-44). A CCR-3 cDNA
CC clone (T31335) was also isolated, and a consensus sequence is
```


XX Human: adenosine receptor; low adenosine antisense oligonucleotide;
KM phosphocholate; impaired respiration; inflammation; allergy;
KM allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;
KM antiallergic; antiaesthetic; cytostatic; analgesic; impaired airway;
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US17712.
XX
XX 03-AUG-1998; 98US-0095212.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX
XX Disclosure: Page 1103; 1343pp; English.
XX
XX The present invention describes a new composition comprising an
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have anti-inflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,
CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC the ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA3213 to AAA5312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680
CC (AAA32323 to AAA33992) are specifically claimed ONs from the present
CC invention. N.B. Sequences given in the disclosure of the present
CC invention do not match up with their corresponding SEQ ID NO: sequences
CC given in the sequence listing.
XX
XX Sequence 1689 BP: 430 A: 416 C: 345 G: 497 T: 1 other:
SQ
Query Match 84.9%; Score 380.4; DB 21; Length 1689;
Best Local Similarity 98.4%; Pred. No. 1.5e-87;
Matches 436; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

OY 126 GACACTGAATATACACAGCAGTAGCATGTATGATACCTTAAGTCAATTACAC 185
DB 1370 GACACTGAATATATACACAGCAGTAGCATGTATGATACCTTAAGTCAATTACAC 1429
OY 186 AGCCAGGAGGCGGCGAGGCTCATCATCAACCTAAAGAGAGCTTGCTTCT 245
DB 1430 AGGCCA-GGGCGGGCAGGCTCATCATCAACCTAAAGAGAGCTTGCTTCT 1487
OY 246 CTTCAAAATGAGTTGCTCATTTAATGACCTGATGTGATGATGATGATG 305
DB 1488 CTTCAAAATGAGTTGCTCATTTAATGACCTGATGTGATGATGATGATG 1547
OY 306 CTCAAAAAGGTAACCTTTTATATTTATATATTAATCTGACGAGCTATGATTA 365
DB 1548 CTCAAAAAGGTAACCTTTTATATTTATATATTAATCTGACGAGCTATGATTA 1606
OY 366 ATAAACATTTTCACACATTAATTAATGATTAATTTTCTAATGCTTATG 425
DB 1607 ATAAACATTTTCACACATTAATTAATGATTAATTTTCTAATGCTTATG 1666
OY 426 TTTCCCTGCTTAATGAAAGCTT 448
DB 1667 TTTCCCTGCTTAATGAAAGCTT 1689

RESULT 11
AB140462
ID AB140462 standard: cDNA; 1689 BP.
XX
XX AB140462;
XX
XX 10-JUN-2002 (first entry)
XX
XX Human C-C chemokine receptor 3 (CCR3) protein encoding cDNA.
XX
XX Mucosae-associated epithelial chemokine; MEC; C-C chemokine receptor;
KM CCR3; CCR10; anti-inflammatory; cytostatic; immunomodulator; anti-viral;
KM antibacterial; chemokine; human; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 181..1248
FT /*tag= a
FT /product= "CCR3"
XX
XX WO200214532-A2.
XX
XX 21-FEB-2002.
XX
XX 15-AUG-2001; 2001WO-US25734.
XX
XX 15-AUG-2000; 2000US-0638914.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Butcher EC, Kunkel EJ, Pan J, Soler-Ferran D;
PI WPI; 2002-269204/31.
XX
XX P-PSDB; ABB07733.
XX
XX Identifying modulators of mucosae-associated epithelial chemokine (MEC)
PT receptors 3 or 10 (CCR3/10), useful for treating inflammatory diseases,
PT comprises detecting formation of MEC-CCR3/10 complex or modulation of a
PT MEC-induced response -
XX
XX Example 2; Fig 4A-B; 92pp; English.
XX
XX The invention relates to identifying agents that inhibit or promote the
CC binding of a mammalian mucosae-associated epithelial chemokine (MEC) to
CC a mammalian C-C chemokine receptor 3 (CCR3) or 10 (CCR10). The method
CC involves: (a) detecting or measuring the formation of a complex between

KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001MO-EP07537.
 XX
 PR 30-JUN-2000; 2000DE-1032529.
 XX 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 XX
 PS Claim 1: SEQ ID NO 310; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX
 SO Sequence 7201 BP; 2131 A; 65 C; 1603 G; 3402 T; 0 other:
 Query Match 75.7%; Score 339.2; DB 24; Length 7201;
 Best Local Similarity 84.8%; Pred. No. 7.5e-77;
 Matches 380; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
 1 TAGGTGAGTGCAGAAATATGCGTAAGAGGAGGAGGAGTGAACCAACACATT 60
 1105 TAAATCAATATACAAAATATACCTAAATAAACCATAAATAAACAACACACATT 1046
 61 AAGCCTTCACACTCACCCTTAAACAGTCCTTCAAACTTCCAGTGCACACTGAAGCTC 120
 1045 AAGCTTCACACTCACCCTTAAACAGTCTTCAAACTTCCAGTGCACACTGAAGCTC 986
 121 TTGAAGACACTGAATATATACACAGCAGTAGATGATGATGATGATGATGATGATGAT 180
 985 TTAAAAACACTAAATATATACACACACACAAATACAAATACAAATATATATATATAT 926
 181 ACCAGAGCCAGGGGCTGGGCGTACATCATCAACCTTAAACAGGAGGAGGAGGAGGAGG 240
 925 ACCAGAGCCAGGGGCTGGGCGTACATCATCAACCTTAAACAGGAGGAGGAGGAGGAGG 866
 241 TCT 300
 865 TCT 806
 301 TGGCGCTACAAAAAGTAAGTATATATATATATATATATATATATATATATATATATAT 360
 805 TACCGCTACAAAAAGTAT 746
 361 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
 745 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 686
 421 AGTTCCTTCCT 448
 685 AATTCTTCCCTACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 658

RESULT 15
 ABL32336
 ID ABL32336 standard; DNA; 7201 BP.
 XX
 AC ABL32336;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 309.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antihaemic; cytosolic; noctropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN MO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001MO-EP07537.
 XX
 PR 30-JUN-2000; 2000DE-1032529.
 XX 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation -
 XX
 PS Claim 1: SEQ ID NO 309; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX
 SO Sequence 7201 BP; 2074 A; 65 C; 1393 G; 3669 T; 0 other:
 Query Match 65.7%; Score 294.4; DB 24; Length 7201;
 Best Local Similarity 78.6%; Pred. No. 2.1e-65;
 Matches 352; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
 1 TAGGTGAGTGCAGAAATATGCTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
 6097 TAGGTGAGTGCAGAAATATGCTTAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6156
 61 AAGCCTTCACACTCACCCTTAAACAGTCCTTCAAACTTCCAGTGCACACTGAAGCTC 120
 6157 AAGTTCCTTCCT 6216
 121 TTGAAGACACTGAATATATACACAGCAGTAGATGATGATGATGATGATGATGATGAT 180
 6217 TTGAAGATATGAAT 6276
 181 ACCAGAGCCAGGGGCTGGGCGTACATCATCAACCTTAAACAGGAGGAGGAGGAGGAGG 240
 6277 AATTAGGTTAGGGGCTGGGCGTACATCATCAACCTTAAACAGGAGGAGGAGGAGGAGG 6336

QY	241	TCCTCTCTAAATGAGTTCCACACTTTTAATGACCCGATTTAGTGGTACCTTA	300
QY	6337	TTTTTTTTTAAATGACTTTTATATTTTTTAATGTATTTGAATGTAGTATGTTATTA	6396
QY	301	TGCCGCTACAAAAGGTAAACTTTTATATTTTATACATTTACCTTCAGCCAGCATTTGA	360
Db	6397	TGTCGTTATATAAAGTAAATTTTATATTTTATATATTTTAAATTTTGTAGTATTTGA	6456
QY	361	TATTAATATAAAACATTTTCACACAATACATTAAGTTAACTATTTTATTTCTTAATGTGCTT	420
Db	6457	TATATAATAAATAATATTTTATATATATTAATTAAGTTAATATATTTTATTTTAAATGTGTTT	6516
QY	421	AGTCTCTCCCTGCTTATATAAAGCTT	448
Db	6517	AGTTTTTTTTTTGTATATCAAAAGTTT	6544

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Job time : 132.328 secs

